

Fig. 1.

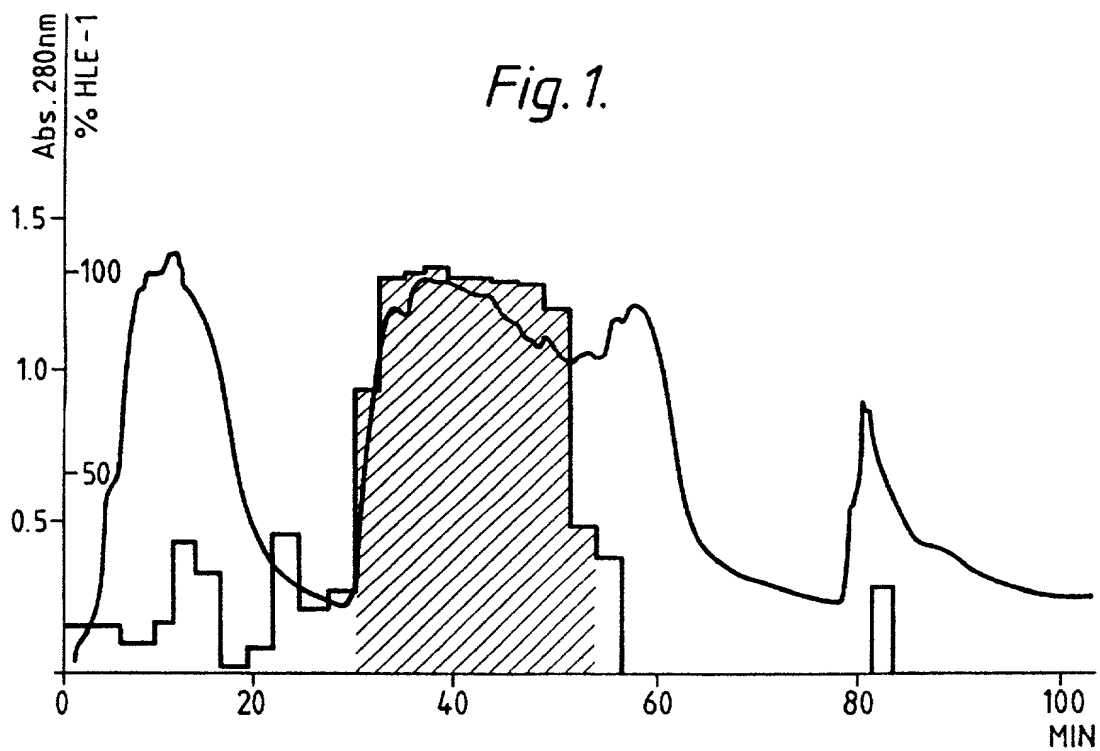


Fig. 2.

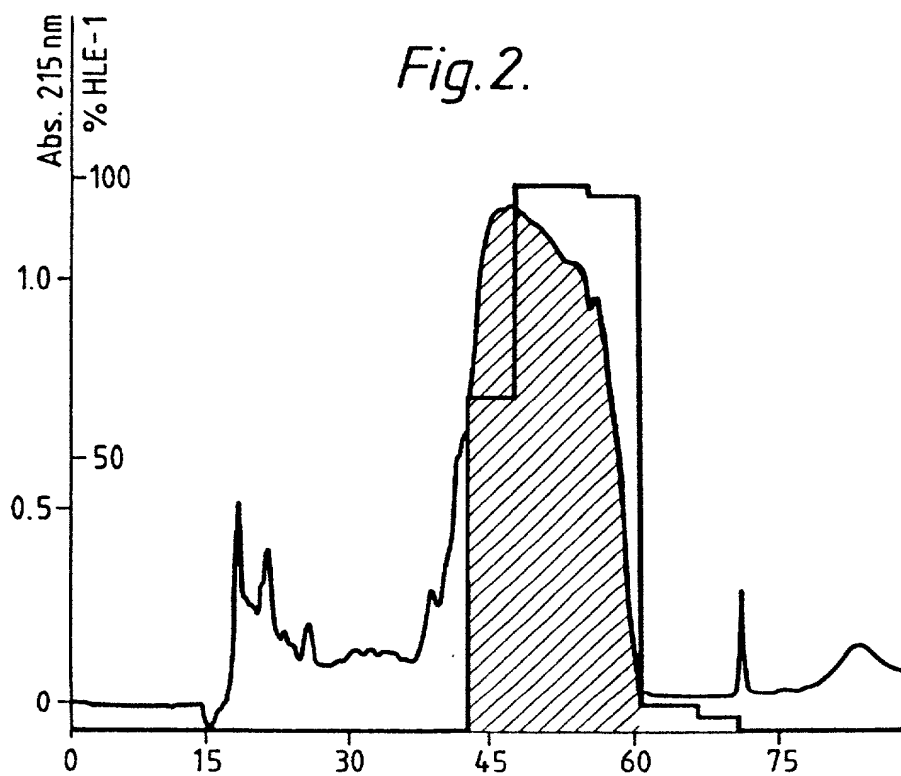


Fig.3.

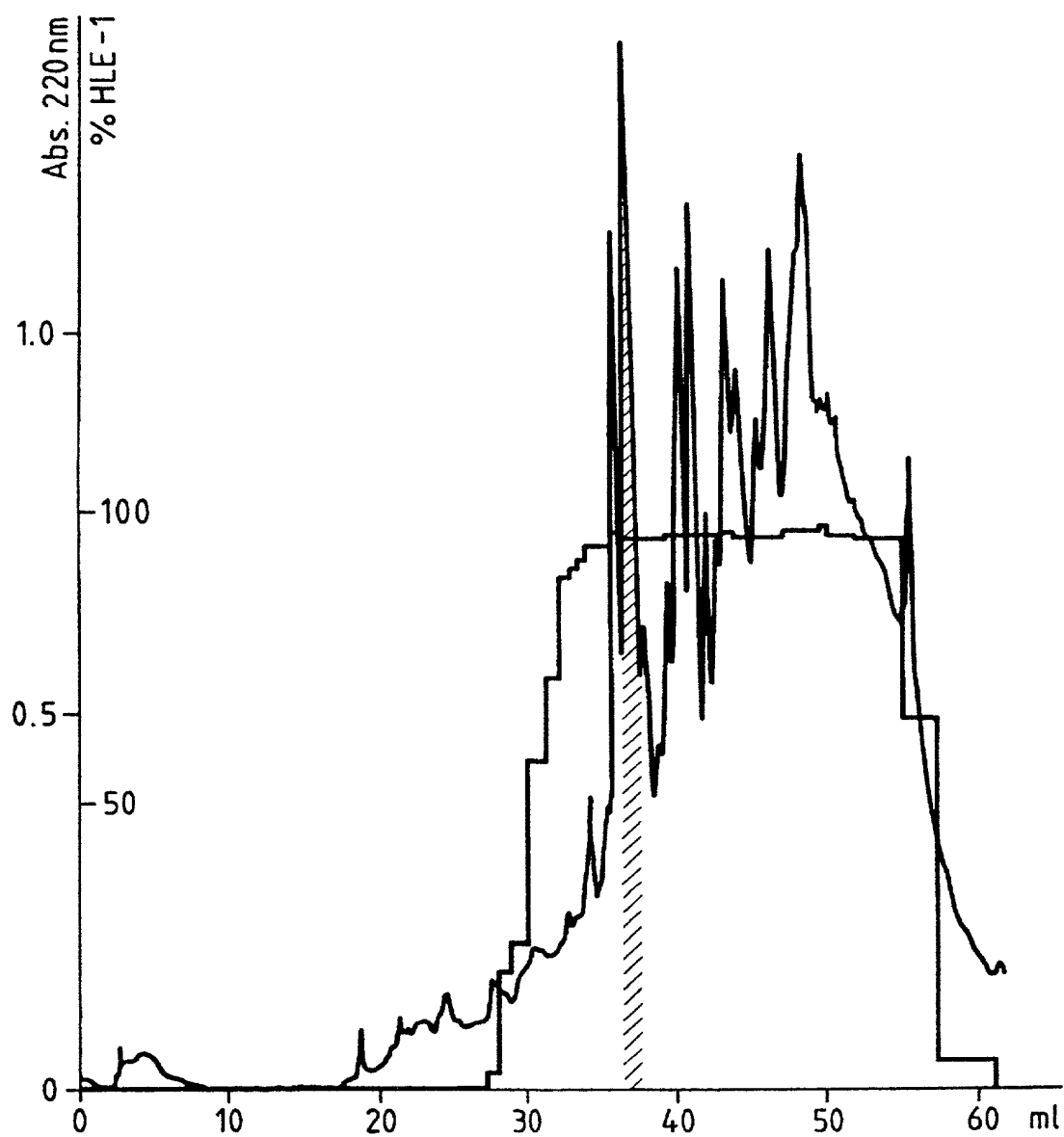
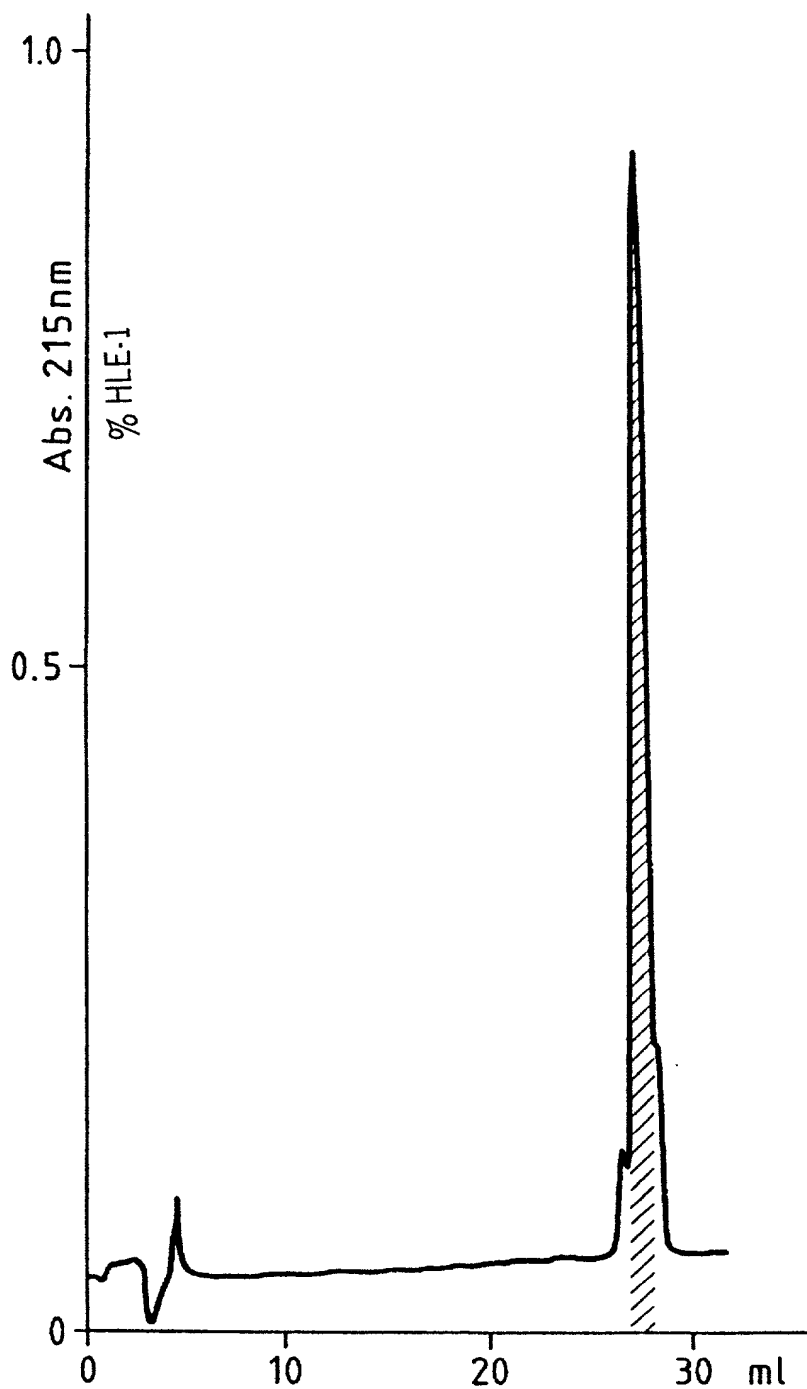
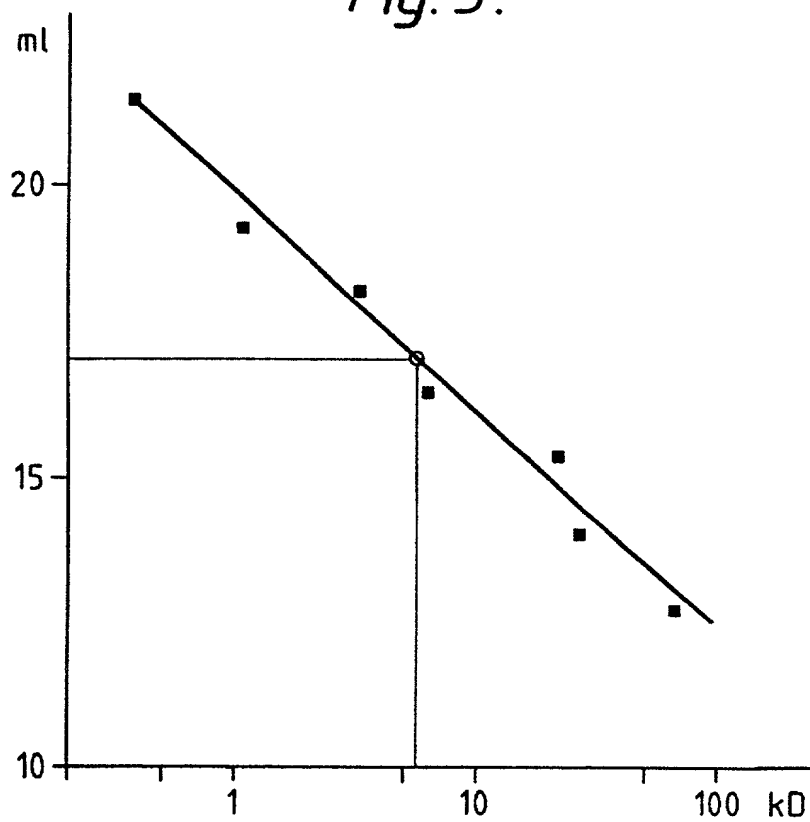


Fig. 4.



*Fig. 5.*



*Fig. 7.*

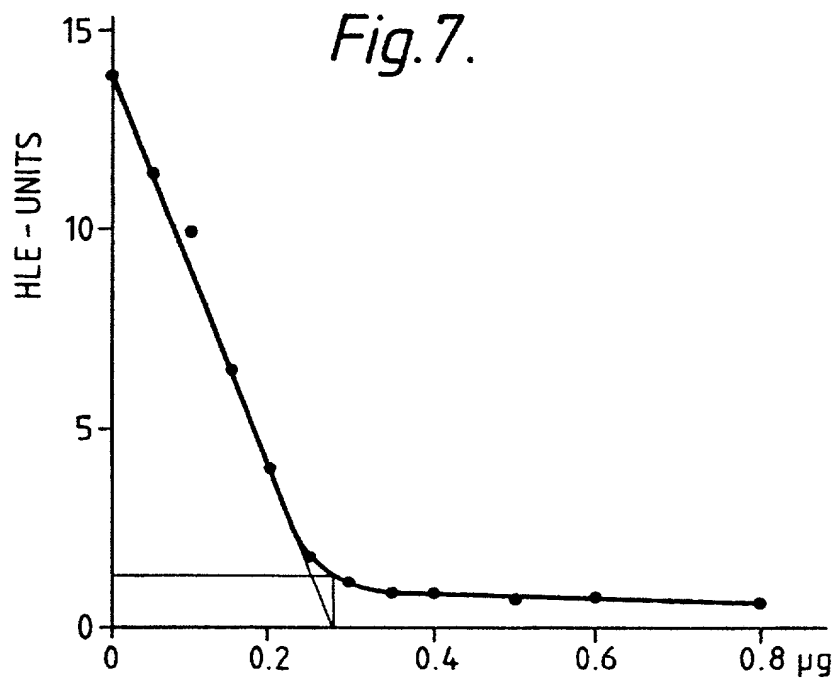


Fig.6.

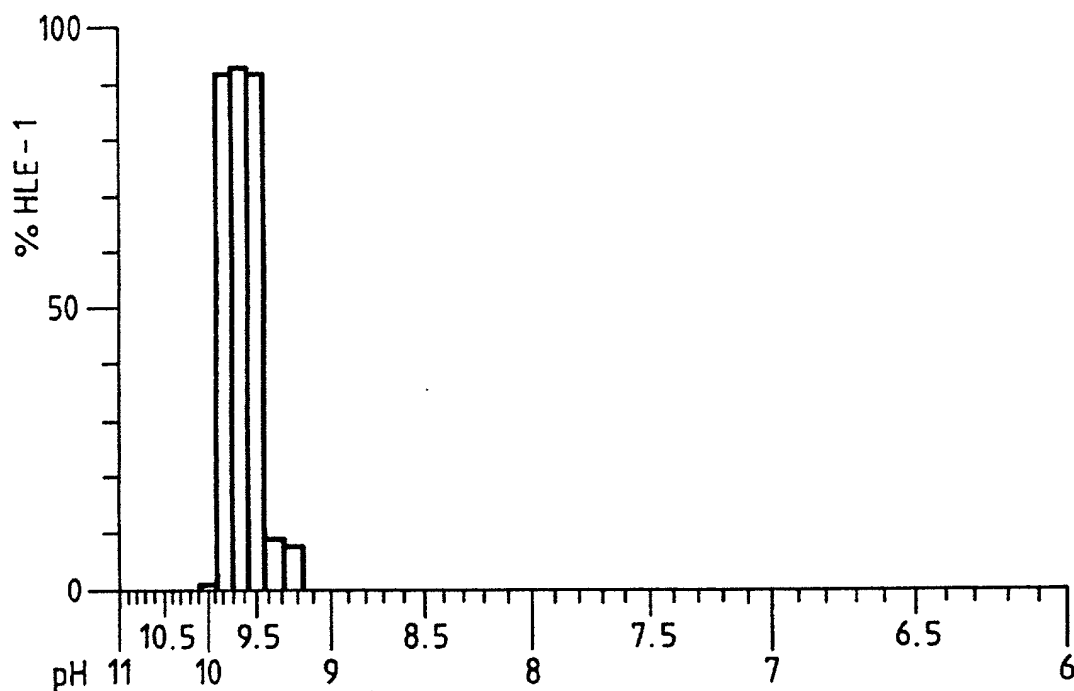
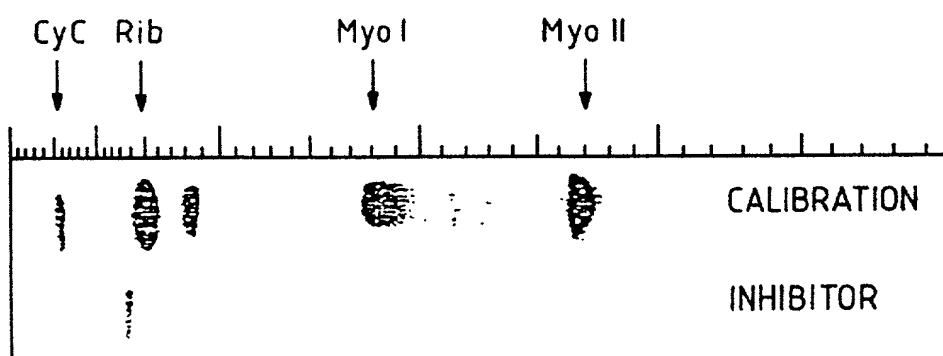




Fig. 9.

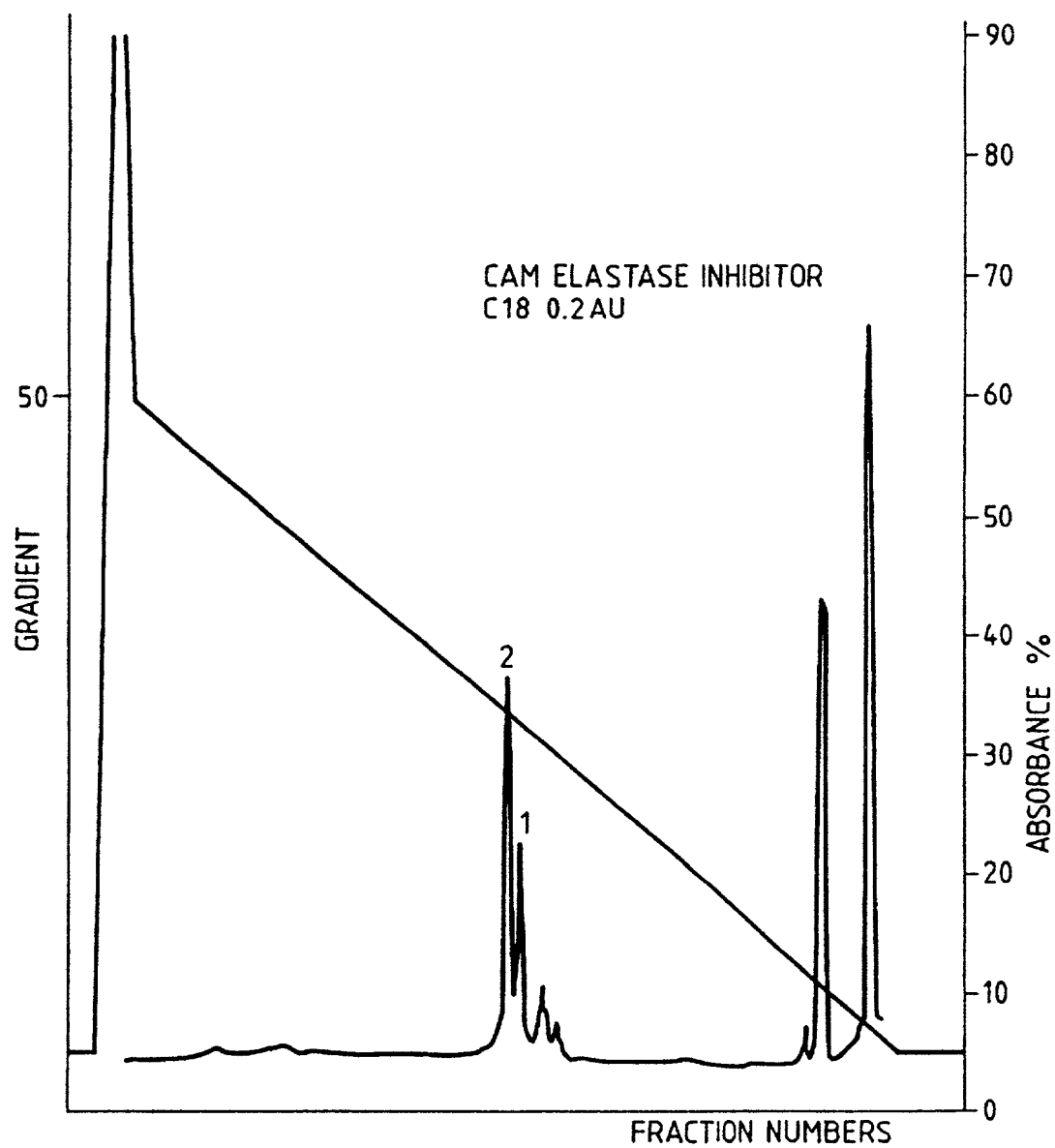


Fig. 10.

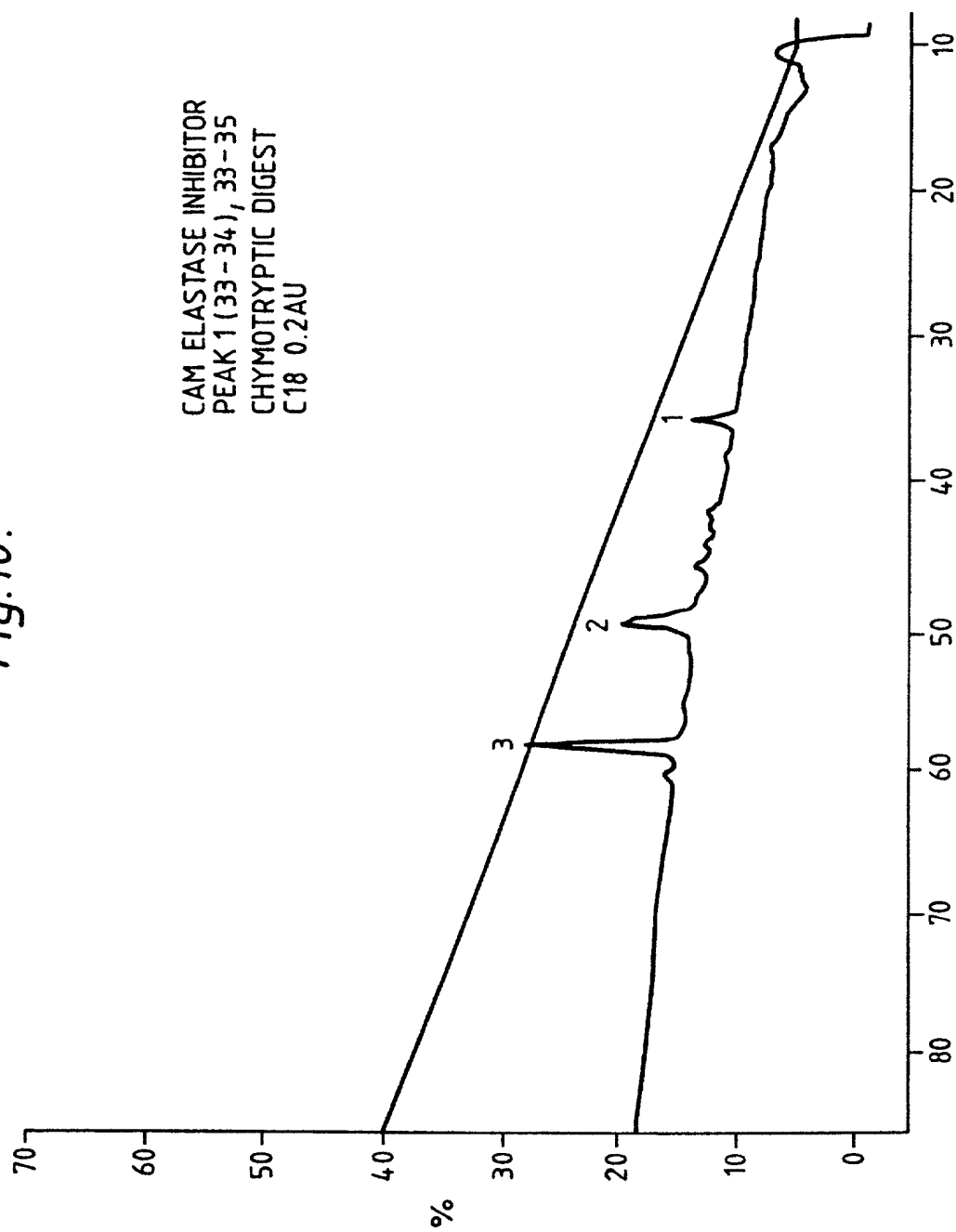
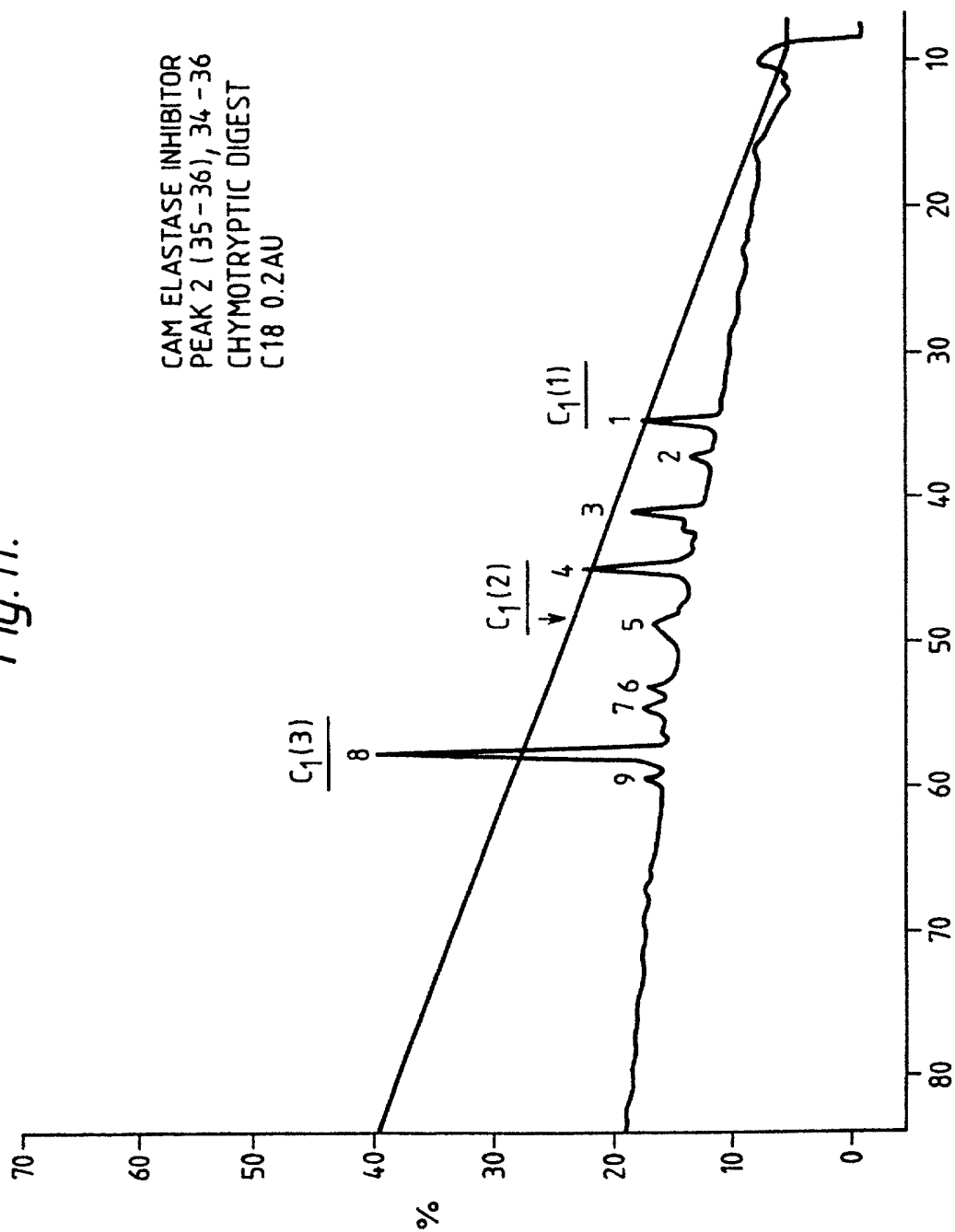




Fig. 11.

CAM ELASTASE INHIBITOR  
PEAK 2 (35-36), 34-36  
CHYMOTRYPTIC DIGEST  
C18 0.2AU



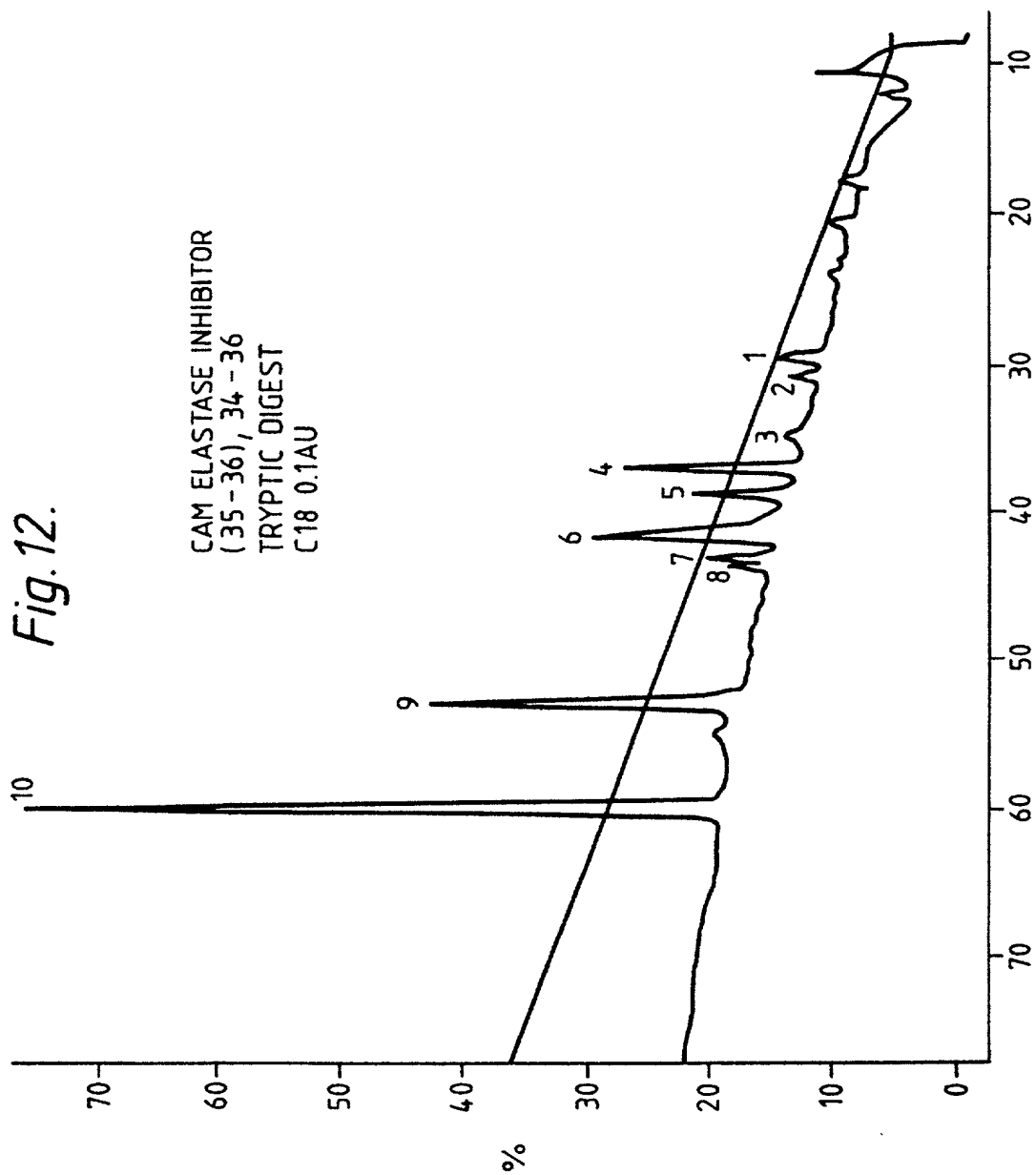


Fig. 13.

AlaGlnGluProValLysGlyProValSerThr

1      ELI1  
AATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACT  
GCTCGAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGA

LysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnProProAsnArg

63      ELI3  
AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT  
TTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCA  
ELI2

CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMet

123      ELI5  
TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCTGCGGTATG  
ACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATAC  
ELI4

AlaCysPheValProGlnEndEnd

183 GCTTGTTTCGTTCCACAATAATAG

CGAACAAAGCAAGGTGTTATTATCCTAG 210  
ELI6

*Fig. 14.*

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys  
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC

5' DNA

Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys  
CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

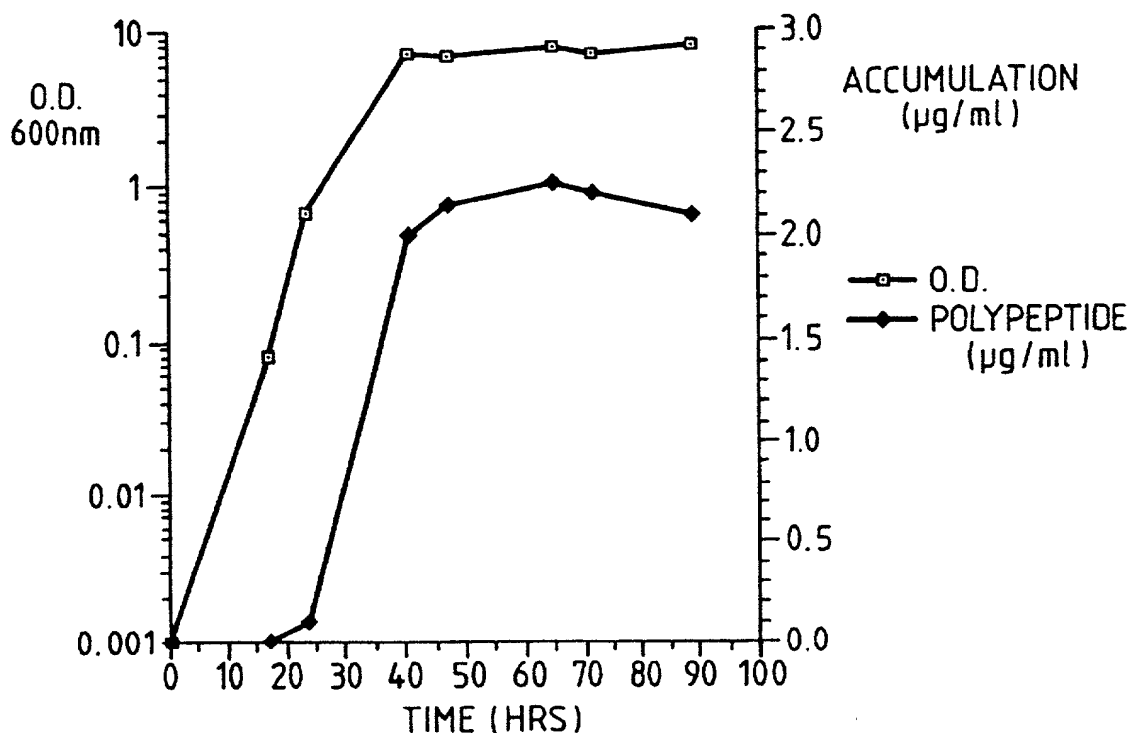
Cys Gly Met Ala Cys Phe Val Pro Gln

TGC GGG ATG GCC TGT TTC GTT CCC CAG

Z = T, C or A

P = A or G

*Fig. 19.*



## Fig. 15.

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys  
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC  
5' DNA

Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys  
CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln  
TGC GGG ATG GCC TGT TTC GTT CCC CAG TAG GAGGGAGCCGGTCCTTGCTGCACCTGT

GCCGTCCCCAGAGCTACAGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCACACTGTCCA  
TTCTTCCTCCCATTGAGGATGCCCCACGGCTGGAGCTGCCTCTCTCATCCACTTTCCAATAAAGAGTTCCG  
GAATTC

Poly A 3'

signal

Z = T, C or A

P = A or G

*Fig. 16.*

10 30 50

. . . . .

GGAATTCCGGTTCCTCATCGCTGGGACGCTGGTTCTAGAGGCAGCTGTCACGGGAGTTCC

EcoRI XbaI

F L I A G T L V L E A A V T G V P

|-----IN-FRAME UPSTREAM PROTEIN SEQUENCE-----

70 90 110

. . . . .

TGTTAAAGGTCAAGACACTGTCAAAGGCCGTGTTCCATTCAATGGACAAGATCCCGTTAA

V K G Q D T V K G R V P F N G Q D P V K

130 150 170

. . . . .

AGGACAAGTTTCAGTTAAAGGTCAAGATAAAGTCAAAGCGCAAGAGCCAGTCAAAGGTCC

G Q V S V K G Q D K V K

AlaGlnGluProValLysGlyPr

|--ELASTASE INHIBITOR--

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

*Fig. 16 (cont.)*

190 210 230  
AGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTGATCCGGTGCGCCATGTTGAATCC  
oValSerThrLysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnPr

250 270 290  
CCCTAACCGCTGCTTGAAAGATACTGACTGCCCAGGAATCAAGAAGTGCTGTGAAGGCTC  
oProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySe

310 330 350  
TTGCGGGATGGCCTGTTTCGTTCCCCAGTGAGAGGGAGCCGGTCCTTGCTGCACCTGTGC  
rCysGlyMetAlaCysPheValProGlnEnd

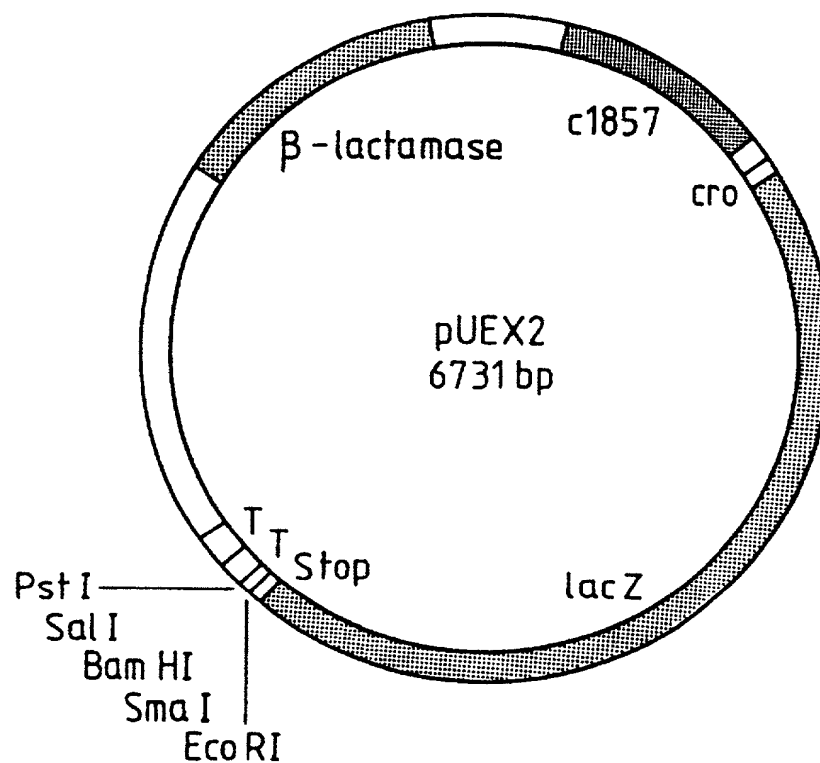
370 390 410  
CGTCCCCAGAGCTACAGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCAC

430 450 470  
ACTGTCCATTCTTCCTCCCATTGAGGATGCCCACGGCTGGAGCTGCCTCTCTCATCCACT

490  
TTCCAATAAAGAGTTCCGGAATTC

Poly A EcoRI  
signal

Fig. 17.



	EcoRI	SmaI	BamHI	SalI		PstI									
pUEX2															
	GAA	TTC	CCG	GGG	ATC	CGT	CGA	CCT	GCA	GCC	AAG	CTT	GCT	GAT	TGA
	Glu	Phe	Pro	Gly	Ile	Arg	Arg	Pro	Ala	Ala	Lys	Leu	Ala	Asp	***



Fig.18.

